

SEQUENCE LISTING

<110> Russell, William
Klaenhammer, Todd

<120> LACTOBACILLUS BETA-GLUCURONIDASE AND DNA ENCODING THE SAME

<130> 5051.514

<150> 60/206,372

<151> 2000-05-23

<160> 14

<170> PatentIn version 3.0

<210> 1

<211> 2150

<212> DNA

<213> Lactobacillus gasseri

<220>

<221> CDS

<222> (153)..(1946)

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agagaaaaca ttactagaaa ggaaaatcat ct atg gaa tct gca cta tat cca	173
Met Glu Ser Ala Leu Tyr Pro	
1 5	
att caa aat aaa tat cgg ttt aac act tta atg aat ggc act tgg caa	221
Ile Gln Asn Lys Tyr Arg Phe Asn Thr Leu Met Asn Gly Thr Trp Gln	
10 15 20	
ttt gaa act gat cct aac tct gtt ggt ctt gac gag gga tgg aat aaa	269
Phe Glu Thr Asp Pro Asn Ser Val Gly Leu Asp Glu Gly Trp Asn Lys	
25 30 35	
gag ttg cct gat cct gaa gaa atg cct gta cca ggt acg ttt gca gaa	317
Glu Leu Pro Asp Pro Glu Glu Met Pro Val Pro Gly Thr Phe Ala Glu	
40 45 50 55	
tta act act aag cga gac cgt aaa tac tat act gga gac ttt tgg tat	365
Leu Thr Thr Lys Arg Asp Arg Lys Tyr Tyr Thr Gly Asp Phe Trp Tyr	
60 65 70	
caa aaa gac ttc ttt att cct tca ttt cta aag aag aaa gaa ctt tat	413
Gln Lys Asp Phe Phe Ile Pro Ser Phe Leu Lys Lys Lys Glu Leu Tyr	
75 80 85	
atc cgt ttt ggt tcg gtt act cat cgc gca aaa gta ttt att aat gga	461
Ile Arg Phe Gly Ser Val Thr His Arg Ala Lys Val Phe Ile Asn Gly	
90 95 100	
cat gaa gtc ggt caa cat gaa ggt ggt ttt tta cca ttt caa gta aaa	509
His Glu Val Gly Gln His Glu Gly Gly Phe Leu Pro Phe Gln Val Lys	

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105	110	115	
att tca aat tat att aat tac gac caa act aat cgt gta act gtt tta			557
Ile Ser Asn Tyr Ile Asn Tyr Asp Gln Thr Asn Arg Val Thr Val Leu			
120	125	130	135
gtc aat aac gaa tta tct gaa aaa gct att cct tgc ggc acc gaa gaa			605
Val Asn Asn Glu Leu Ser Glu Lys Ala Ile Pro Cys Gly Thr Glu Glu			
	140	145	150
atc tta gat aac ggt caa aaa ctt gct caa cct tat ttt gat ttc ttc			653
Ile Leu Asp Asn Gly Gln Lys Leu Ala Gln Pro Tyr Phe Asp Phe Phe			
	155	160	165
aat tat tct ggc att atg cgg aat gtc tgg ctc tta gca ctt cct caa			701
Asn Tyr Ser Gly Ile Met Arg Asn Val Trp Leu Leu Ala Leu Pro Gln			
	170	175	180
agc caa atc act aat ttt aaa cta aat tat caa tta gca aat aat aag			749
Ser Gln Ile Thr Asn Phe Lys Leu Asn Tyr Gln Leu Ala Asn Asn Lys			
	185	190	195
gca aca att acc tac aat atc gag gca aat aat aat gct gaa ttt aaa			797
Ala Thr Ile Thr Tyr Asn Ile Glu Ala Asn Asn Ala Glu Phe Lys			
200	205	210	215
gta aca ctt ttc gat aat caa aaa gaa gta gcg tgt gct act tct aaa			845
Val Thr Leu Phe Asp Asn Gln Lys Glu Val Ala Cys Ala Thr Ser Lys			
	220	225	230
aat act agt agt tta aca att aag aat ccg cac ctt tgg agt cca aac			893
Asn Thr Ser Ser Leu Thr Ile Lys Asn Pro His Leu Trp Ser Pro Asn			
	235	240	245
gat ccg tat tca tac aaa ata aag att gaa atg ctc gaa gac gga aaa			941
Asp Pro Tyr Ser Tyr Lys Ile Lys Ile Glu Met Leu Glu Asp Gly Lys			
	250	255	260
aca gtt gac gaa tac aca gat aaa att ggt atc cgc aca gtt aaa att			989
Thr Val Asp Glu Tyr Thr Asp Lys Ile Gly Ile Arg Thr Val Lys Ile			
	265	270	275
gtg aat gat aaa atc ttg ctc aat aat cac cca att tat tta aaa ggc			1037
Val Asn Asp Lys Ile Leu Leu Asn Asn His Pro Ile Tyr Leu Lys Gly			
280	285	290	295
ttt ggc aag cac gaa gat ttt aat gtt tta ggc aaa gca gtt aac gaa			1085
Phe Gly Lys His Glu Asp Phe Asn Val Leu Gly Lys Ala Val Asn Glu			
	300	305	310
agc att atc aaa cgc gac tac gaa tgc atg aaa tgg att ggc gct aac			1133
Ser Ile Ile Lys Arg Asp Tyr Glu Cys Met Lys Trp Ile Gly Ala Asn			
	315	320	325
tgt ttt aga agc agt cac tat cct tac gcc gaa gaa tgg tat caa tat			1181
Cys Phe Arg Ser Ser His Tyr Pro Tyr Ala Glu Glu Trp Tyr Gln Tyr			
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gcc gat aaa tat ggc ttt tta att att gat gaa gta ccc gct gtt ggt			1229
Ala Asp Lys Tyr Gly Phe Leu Ile Ile Asp Glu Val Pro Ala Val Gly			
	345	350	355
ctt aat cgt tca ata act aac ttt ctt aat gta act aat tct aat cag			1277
Leu Asn Arg Ser Ile Thr Asn Phe Leu Asn Val Thr Asn Ser Asn Gln			
360	365	370	375

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tcg cac ttt ttt gct tcg aaa act gtg cct gaa tta aaa aag gtc cat	1325
Ser His Phe Phe Ala Ser Lys Thr Val Pro Glu Leu Lys Lys Val His	
380 385 390	
gaa caa gaa ata aaa gaa atg atc gat cgc gac cag cgt cac cct tca	1373
Glu Gln Glu Ile Lys Glu Met Ile Asp Arg Asp Gln Arg His Pro Ser	
395 400 405	
gtg att gcc tgg agt tta ttc aat gaa cca gaa tca act act caa gaa	1421
Val Ile Ala Trp Ser Leu Phe Asn Glu Pro Glu Ser Thr Thr Gln Glu	
410 415 420	
tcc tat gac tat ttc aaa gat att ttt gcc ttt gcg aga aaa ttg gat	1469
Ser Tyr Asp Tyr Phe Lys Asp Ile Phe Ala Phe Ala Arg Lys Leu Asp	
425 430 435	
cca caa aat cgt cct tat act gga act tta gtt atg ggt agc ggt cca	1517
Pro Gln Asn Arg Pro Tyr Thr Gly Thr Leu Val Met Gly Ser Gly Pro	
440 445 450 455	
aaa gtg gat aag ctt cac cca ctt tgt gac ttt gtc tgc tta aac cgt	1565
Lys Val Asp Lys Leu His Pro Leu Cys Asp Phe Val Cys Leu Asn Arg	
460 465 470	
tat tat ggt tgg tac gtt gct ggt ggt cct gaa atc gtt aat gct aaa	1613
Tyr Tyr Gly Trp Tyr Val Ala Gly Gly Pro Glu Ile Val Asn Ala Lys	
475 480 485	
aag atg ctg gaa gat gaa cta gac ggc tgg caa aac tta aag ctt aat	1661
Lys Met Leu Glu Asp Glu Leu Asp Gly Trp Gln Asn Leu Lys Leu Asn	
490 495 500	
aaa cca ttt gtc ttt act gag ttt ggc gct gat aca tta tct tct tct	1709
Lys Pro Phe Val Phe Thr Glu Phe Gly Ala Asp Thr Leu Ser Ser Ser	
505 510 515	
cat cgc ctt cca gat gaa atg tgg agc caa gaa tat caa aat gaa tat	1757
His Arg Leu Pro Asp Glu Met Trp Ser Gln Glu Tyr Gln Asn Glu Tyr	
520 525 530 535	
tat caa atg tat ttt gat ata ttt aag aaa tat cca ttt att tgt ggc	1805
Tyr Gln Met Tyr Phe Asp Ile Phe Lys Lys Tyr Pro Phe Ile Cys Gly	
540 545 550	
gaa tta gtt tgg aac ttt gct gac ttt aag acg agt gaa gga atc atg	1853
Glu Leu Val Trp Asn Phe Ala Asp Phe Lys Thr Ser Glu Gly Ile Met	
555 560 565	
cgt gtt ggt ggt aac gat aaa gga att ttt act cgc gat cgt gaa cct	1901
Arg Val Gly Gly Asn Asp Lys Gly Ile Phe Thr Arg Asp Arg Glu Pro	
570 575 580	
aaa gat att gcc ttt acc ttg aaa aag aga tgg caa caa tta aat	1946
Lys Asp Ile Ala Phe Thr Leu Lys Lys Arg Trp Gln Gln Leu Asn	
585 590 595	
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tcatttgata tcgattatatt gattatgggc gcgatttttt attgattttg ataataattt	2066
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<210> 2
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 <213> Lactobacillus gasseri

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Leu	Met	Asn	Gly	Thr	Trp	Gln	Phe	Glu	Thr	Asp	Pro	Asn	Ser	Val	Gly	20	25	30	
Leu	Asp	Glu	Gly	Trp	Asn	Lys	Glu	Leu	Pro	Asp	Pro	Glu	Glu	Met	Pro	35	40	45	
Val	Pro	Gly	Thr	Phe	Ala	Glu	Leu	Thr	Thr	Lys	Arg	Asp	Arg	Lys	Tyr	50	55	60	
Tyr	Thr	Gly	Asp	Phe	Trp	Tyr	Gln	Lys	Asp	Phe	Phe	Ile	Pro	Ser	Phe	65	70	75	80
Leu	Lys	Lys	Lys	Glu	Leu	Tyr	Ile	Arg	Phe	Gly	Ser	Val	Thr	His	Arg	85	90	95	
Ala	Lys	Val	Phe	Ile	Asn	Gly	His	Glu	Val	Gly	Gln	His	Glu	Gly	Gly	100	105	110	
Phe	Leu	Pro	Phe	Gln	Val	Lys	Ile	Ser	Asn	Tyr	Ile	Asn	Tyr	Asp	Gln	115	120	125	
Thr	Asn	Arg	Val	Thr	Val	Leu	Val	Asn	Asn	Glu	Leu	Ser	Glu	Lys	Ala	130	135	140	
Ile	Pro	Cys	Gly	Thr	Glu	Glu	Ile	Leu	Asp	Asn	Gly	Gln	Lys	Leu	Ala	145	150	155	160
Gln	Pro	Tyr	Phe	Asp	Phe	Phe	Asn	Tyr	Ser	Gly	Ile	Met	Arg	Asn	Val	165	170	175	
Trp	Leu	Leu	Ala	Leu	Pro	Gln	Ser	Gln	Ile	Thr	Asn	Phe	Lys	Leu	Asn	180	185	190	
Tyr	Gln	Leu	Ala	Asn	Asn	Lys	Ala	Thr	Ile	Thr	Tyr	Asn	Ile	Glu	Ala	195	200	205	
Asn	Asn	Asn	Ala	Glu	Phe	Lys	Val	Thr	Leu	Phe	Asp	Asn	Gln	Lys	Glu	210	215	220	
Val	Ala	Cys	Ala	Thr	Ser	Lys	Asn	Thr	Ser	Ser	Leu	Thr	Ile	Lys	Asn	225	230	235	240
Pro	His	Leu	Trp	Ser	Pro	Asn	Asp	Pro	Tyr	Ser	Tyr	Lys	Ile	Lys	Ile	245	250	255	
Glu	Met	Leu	Glu	Asp	Gly	Lys	Thr	Val	Asp	Glu	Tyr	Thr	Asp	Lys	Ile	260	265	270	
Gly	Ile	Arg	Thr	Val	Lys	Ile	Val	Asn	Asp	Lys	Ile	Leu	Leu	Asn	Asn	275	280	285	
His	Pro	Ile	Tyr	Leu	Lys	Gly	Phe	Gly	Lys	His	Glu	Asp	Phe	Asn	Val	290	295	300	

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Leu Gly Lys Ala Val Asn Glu Ser Ile Ile Lys Arg Asp Tyr Glu Cys
 305 310 315 320
 Met Lys Trp Ile Gly Ala Asn Cys Phe Arg Ser Ser His Tyr Pro Tyr
 325 330 335
 Ala Glu Glu Trp Tyr Gln Tyr Ala Asp Lys Tyr Gly Phe Leu Ile Ile
 340 345 350
 Asp Glu Val Pro Ala Val Gly Leu Asn Arg Ser Ile Thr Asn Phe Leu
 355 360 365
 Asn Val Thr Asn Ser Asn Gln Ser His Phe Phe Ala Ser Lys Thr Val
 370 375 380
 Pro Glu Leu Lys Lys Val His Glu Gln Glu Ile Lys Glu Met Ile Asp
 385 390 395 400
 Arg Asp Gln Arg His Pro Ser Val Ile Ala Trp Ser Leu Phe Asn Glu
 405 410 415
 Pro Glu Ser Thr Thr Gln Glu Ser Tyr Asp Tyr Phe Lys Asp Ile Phe
 420 425 430
 Ala Phe Ala Arg Lys Leu Asp Pro Gln Asn Arg Pro Tyr Thr Gly Thr
 435 440 445
 Leu Val Met Gly Ser Gly Pro Lys Val Asp Lys Leu His Pro Leu Cys
 450 455 460
 Asp Phe Val Cys Leu Asn Arg Tyr Tyr Gly Trp Tyr Val Ala Gly Gly
 465 470 475 480
 Pro Glu Ile Val Asn Ala Lys Lys Met Leu Glu Asp Glu Leu Asp Gly
 485 490 495
 Trp Gln Asn Leu Lys Leu Asn Lys Pro Phe Val Phe Thr Glu Phe Gly
 500 505 510
 Ala Asp Thr Leu Ser Ser Ser His Arg Leu Pro Asp Glu Met Trp Ser
 515 520 525
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 530 535 540
 Lys Tyr Pro Phe Ile Cys Gly Glu Leu Val Trp Asn Phe Ala Asp Phe
 545 550 555 560
 Lys Thr Ser Glu Gly Ile Met Arg Val Gly Gly Asn Asp Lys Gly Ile
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<210> 3
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<223> Synthetic Oligonucleotide Primer.

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